



032301.202.seq.ST25.txt
SEQUENCE LISTING

<110> BATHE, Brigitte

<120> NUCLEOTIDE SEQUENCES CODING FOR THE sigC GENE

<130> 032301 WD 202

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1109

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (300)..(878)

<223>

<400> 1

tggaaactgg tgcgggtgtt ggcgggttgtt gtttccagaa agctttggac gcattccgcg 60

atctacgatc tggctcgctg ctgacttctc agacatttgc attccttcct tttatgaggg 120

ttacccatgg attaagtctg attgatagtc tacatcagaa tgtcacttcg cgccacccaaa 180

taatcagccc ttacgtaaac tgccagcaaa aagacaaaag tatgatactt ttgcccact 240

ttgacaccccc ctacacaccc ttatggtgac cccggctctga actggatttc tgagcaatt 299

gtg aag tca aaa gag cgt aac gac gcc cac gtc acc gag ctg gcc cta 347

Met Lys Ser Lys Glu Arg Asn Asp Ala His Val Thr Glu Leu Ala Leu

1 5 10 15

gcc gcc ggc cgt ggc gac cgc gca gct ctc acc gat ttc atc cg 395

Ala Ala Gly Arg Gly Asp Arg Ala Ala Leu Thr Asp Phe Ile Arg Glu

20 25 30

acc caa gac gat gtc tgg cgt ctc ctc gcc cac ctt ggc ggc cac gaa 443

Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly His Glu

35 40 45

atc gcc gac gat cta acc caa gaa act tat ctg cg 491

Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met Ser Ala

50 55 60

ctc ccc cgc ttc gca gcg cgc tcc tcg gcg cgt acc tgg cta cta tcg 539

Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu Leu Ser

65 70 75 80

cta gcc cgg cgc gtc tgg gtc gac aac atc cga cac gac atg gca cgc 587

Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met Ala Arg

85 90 95

ccc cgc aaa tcc atc gtc gaa tac gaa gac acc ggt gcc acc gac gcg 635

032301.202.seq.ST25.txt

Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr Asp Ala		
100	105	110
agc aac gca ggc atc tgg tcc gag tgg atc gac gtg cgc acg ctt atc		683
Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr Leu Ile		
115	120	125
gac gcc ctc cca ccc gaa cgc cgc gaa gcc ctc atc ctc acc caa gtg		731
Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr Gln Val		
130	135	140
ttg ggc tac acc tac gaa gaa gcc gca aaa atc gcc gac gtc cga gtc		779
Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val Arg Val		
145	150	155
gga aca atc cgt tcc cgc gta gcc cgc gcc aga gcg gac ctc att gct		827
Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu Ile Ala		
165	170	175
gca aca gct acc ggt gat tcc tca gcc gaa gat ggc aaa tcc gcc caa		875
Ala Thr Ala Thr Gly Asp Ser Ser Ala Glu Asp Gly Lys Ser Ala Gln		
180	185	190
ggt tagcagatga gctacgtcaa cggcgtaatc ccttaaccag attgctaatt		928
Gly		
tacagttcta ttttgctgct cgatcaaagc gactcttacc caccctagaa tcctttgacc		988
gcataaacac tttgtttta tctaaaactg aatcttaat ttttacgctc gcagatgatt		1048
ttcctccagc aatggaagta ataaccccgc cccgaacgac agctttcga ggtgcgccttc		1108
c		1109

<210> 2
 <211> 193
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 2

Met Lys Ser Lys Glu Arg Asn Asp Ala His Val Thr Glu Leu Ala Leu		
1	5	10
		15

Ala Ala Gly Arg Gly Asp Arg Ala Ala Leu Thr Asp Phe Ile Arg Glu		
20	25	30

Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly His Glu		
35	40	45

Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met Ser Ala		
50	55	60

032301.202.seq.ST25.txt

Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu Leu Ser
65 70 75 80

Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met Ala Arg
85 90 95

Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr Asp Ala
100 105 110

Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr Leu Ile
115 120 125

Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr Gln Val
130 135 140

Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val Arg Val
145 150 155 160

Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu Ile Ala
165 170 175

Ala Thr Ala Thr Gly Asp Ser Ser Ala Glu Asp Gly Lys Ser Ala Gln
180 185 190

Gly

<210> 3
<211> 28
<212> DNA
<213> Corynebacterium glutamicum

<400> 3
acggtaaaaaa ctacacacacct ttatggtg

28

<210> 4
<211> 28
<212> DNA
<213> Corynebacterium glutamicum

<400> 4
gctctagagt tgacgttagct catctgct

28